"genetic locus" as including a gene that encodes a protein including any upstream or downstream transcribed noncoding regions and associated regulatory regions.

The addition of new claims 26 and 29, reciting haplotype determination by detecting polymorphisms in coding and non-coding regions, is supported at least by original claim 12 and by the specification at least at pg. 8, lines 4-6 which recites that "intron sequences provide genetic variations that, in addition to those found in exon sequences, further distinguish sample DNA...." Additionally, pg. 16, lines 13-16 specifies that the amplified sequence to be analyzed "preferably includes at least a portion of one of the introns adjacent to a variable exon and can include a portion of the variable exon. When additional sequence information is required, the amplified DNA sequence preferably encompasses a variable exon and all or a portion of both adjacent intron sequences." At pg. 21, lines 19-24 the specification discloses various types of polymorphisms used to distinguish the haplotypes of the DQA1 locus.

The addition of new claims 27, 28 and 30, reciting non-coding regions comprising an intervening sequence, 5'-UTR, 3'-UTR, a regulatory sequence or an intergenic sequence is supported in the specification at least at pg. 9, lines 29-35 which recites that the term "intron" refers to untranslated DNA sequences between exons (i.e., intervening sequences), together with 5' and 3' untranslated regions associated with a genetic locus and intergenic spacing sequences. The new claims are further supported at pg. 10, lines 5-8, which defines an "intervening sequence" and at pg. 15, lines 20-22 which discusses "highly conserved intron regions, e.g., promoters, operators and other DNA regulatory regions."

The amendments and new claims are added to further clarify the scope of the claimed invention and not for any reasons related to patentability of the subject matter.

Applicants respectfully submit that the amendments to claims 1, 13 and 19 and addition of new claims 26-30 do not introduce new subject matter.

Charge our Deposit Account

It is believed that no fee is due as a result of the Preliminary Amendment. However, if any fee is due, please charge any shortage to our Deposit Account No. 02-2666.

Respectfully submitted,
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Appendix A: Amendment to Specification

This application is a continuation of application serial No. 09/070,497; which was a continuation of application serial No. 07/949,652, now U.S. Patent No. 5,612,179; which was a continuation of application serial No. 07/551,239, now U.S. Patent No. 5,192,659; which was a continuation of 07/550,939, abandoned; which was a continuation of 07/465,863, abandoned; which was a continuation of 07/405,499, abandoned; which was a continuation of 07/398,217, abandoned.

APPENDIX B: Amendments to Claims

1. (Amended) A method of determining at least one haplotype of a genetic coding locus comprising:

(a) amplifying genomic DNA, wherein the amplified genomic DNA comprises a non-coding region sequence that is in genetic linkage with the genetic coding locus;

(b) detecting one or more sequence variations in the non-coding region; and

(c) determining at least one haplotype of the genetic coding locus.

13. (Amended) A method for determination of at least one haplotype of a multi-allelic genetic coding locus comprising:

(a) amplifying genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said genetic coding locus and contains a sufficient number of non-coding region sequence nucleotides to produce an amplified DNA sequence characteristic of said at least one haplotype;

(b) analyzing the amplified DNA sequence; and

(c) determining at least one haplotype of the multiallelic genetic coding locus.

19. (Amended) A method for determination of at least one haplotype of an HLA coding locus comprising:

(a) amplifying genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said [genetic] HLA coding locus [and contains a

sufficient number of non-coding region sequence nucleotides to produce an amplified DNA sequence characteristic of said at least one haplotype];

(b) analyzing the amplified DNA sequence; and

(c) determining at least one haplotype of the HLA coding locus.

26. (New) The method of claim 1, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

27. (New) The method of claim 1, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

28. (New) The method of claim 13, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

29. (New) The method of claim 19, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

30. (New) The method of claim 19, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.